

QY 263 QNLISGGIYPTKPPGDPMPMPNQPTSVLIRKYAIDYISK----- 305
 Db 481 D-----VNTEKELT-----DYNQYLOKITYGDNNSAVIDFGNADSAVYVMN 522
 QY 306 -----LLEGATVQLTGD----- 319
 Db 523 TKFQQTNSNTEPSTLWQMATLSSTGKVSYSTGNALGFTNNQSGGAGQEVYVIGNYWEDTK 582
 QY 320 NSFQ-----ARVFSN---DIGERIELDGTYLTEL-----NSPAGS 355
 Db 583 NGVQBLGEKGVGNTVTVTDNNTNPKVGRVTKEDGSYLLPNLNGDYRVEFSNLPKGE 642
 QY 355 IAE----- 358
 Db 643 VTPSKQGNHNEBLSNGLSSVTNGKDNLSADLGTYKPKYNLSDYVWEDTNKNGIODE 702
 QY 359 -----PIFKVKEAGKVY---TIDGK---QENPNEI-----WEPYSVEAYNDF 397
 Db 703 KGISGTVVTLKDENGVLTVTADGKFTDLDNGNQVKEFVTPPEGPTVTSGR 762
 QY 398 EEFs- VLTTONY-----AKFYYAKNKGSSQVVCNFNADLKSPPDSED--GGT 443
 Db 763 EKDSNLTTGTINGADNMTLDGSFVYKTKYKLNGLNYWEDTNKDGQ- DSTERGISGVT 820
 QY 444 MTPDFTGKVYKTHLAGR-LFKTYVKPDTDPDTFLKIKVIEKGYFEGQALY -- 499
 Db 821 VTLKNENGEVLQTKTDKGKQY-----GLNGTYKVEFEP 859
 Qy 500 SGLTETQLAATOLAI-YFTDSAELDK-----LKDY-----HGFG 536
 Db 860 SGYPTQVSGTDBGIDSNGTSTGTVIKDKNDTDSGFYKPTVNLGDYVWEDTNKNGQ 919
 QY 537 DMNDSTLAVA-----KILVEYAQDSNPP-OLTDLDFIPNNKQSLIGTQWHPED 586
 Db 920 DKDKEKGISCVTVTLKDENDKVKLVTIDNGKQFTDL-----NNCTYK- 963
 QY 587 LVDITRMEKKEVIP---VHNHLTURK-----TVGLG--AGDRKDFHEIELKNKQBL 636
 Db 964 ---VEFEPSPGIFTSTVTSVGSNDTEKDSMGLTGVIKDADNMTLDSGF--YKTPKYL 1016
 QY 637 -----LSQTVKDNTNEFCKKATINLKHGSLSLTQGLPCESYLVKETSEGYK 689
 Db 1017 GDYYWYDSRKGDKDOSTERKGIVKVTLINEKEGVIGT-----TQDENGKCYCDPNLDSGKVKYV 1076
 QY 690 VNSOEVANAVSKIGTSSETLAFENKNEPVVPTGVQDQKI-NGY 732
 Db 1077 F-EKPGAGLQTQGTNTTEDKDADGGEVYVITDHDFLDNGY 1118

RESULT 2
 US-10-615-383-10
 Sequence 10, Application US/10615383
 GENERAL INFORMATION:
 APPLICANT: FOSNER, Timothy
 TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE STAPHYLC
 FILE REFERENCE: P0635US03/BAS
 CURRENT APPLICATION NUMBER: US/10-615, 383
 CURRENT FILING DATE: 2003-07-09
 PRIOR APPLICATION NUMBER: 09-3786, 962
 PRIOR FILING DATE: 1999-08-31
 PRIOR APPLICATION NUMBER: 60-098, 443
 PRIOR FILING DATE: 1999-01-25
 NUMBER OF SEQ ID NOS: 39
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 10
 LENGTH: 930
 TYPE: PPT
 ORGANISM: *Staphylococcus epidermidis*
 US-10-615-383-10

Query Match 3.68; Score 142; DB 6; Length 930;

Best Local Similarity 18.6%; Pred. No. 0.039; Matches 161; Conservative 131; Mismatches 295; Indels 278; Gaps 42;

Matches 161; Conservative 131; Mismatches 295; Indels 278; Gaps 42;

QY 9 KLNLTNTQR--VLSKNSK---RTVTLGVFLMIFALVTSYMGAKTVFGL-----VES 56
 Db 2 KNNLNUKKPPIANPKNSNKAIRKTVGTSI-----VIGAALFGLGHNKAEE 51
 QY 57 STPNAINPDSSEVRYWYYESVYRGHYYKQFRVAHDLRVNLCGSSRSYQVYCFNLKKAPP 116
 Db 52 NTQDVK-DSNM-----DELSNSDOSSNEERD----VINNSQSI 89
 QY 117 LGSPSSVKK-WYKKHDGISTKEDYAMS-----PRITGDELNOKLRVWMYH 163
 Db 90 TDDDNQIKKEETNSNDAIENRSKDTQSTNTVDENEATFLQKTPQDNTQOLKEEVVKEPSS 149
 QY 164 PONANGIMECLEPLNAINRITQEAWVYWSNAPN- PDESFKRESENUVTSQSLMRQ 222
 Db 150 VENNSMMAQOQSHTTNSIOTSENEENRSVDFANSKTEESNTENKEPTE 209
 Db 223 ALKQLIDPNLATMKRQVDPDFQLSIFESEDKGDKYKQYQNLISGGLVPTKPTPGDP 282
 Db 210 -----PKVREDSITSQPSSYKNDKEKISQDELL--LPINSEYENKVRP 252
 QY 283 MPPN- QPOTSVLIRKYIYGDYKLLCATLQIYGDYNNNSFARVESSNDIGERIELSD 340
 Db 253 LSTNSAQPSSKRVTVNOLAEO-----GSVNVHLIK- VDQSITEGYDDSD 297
 Qy 341 GTYVTELNSPAGYSSAEPITKVEAGKVYI-TDGKQI----- 378
 Db 298 GTKRAHDAEMLI-IVTVEFDVKSGDMNTVNDKNTVPSDLDFAPIPKDNGSGII 356
 QY 379 -----ENPNEIKEVEFYS- VEAVNDFEEFESVLTQNTQYAKFVYAKN- NGSSQVYCENA 429
 Db 357 ATGTYDNTNKOITYTFTDVYKVENIKAIKLT-----YDTSKVPNNNTKLDEVKT 410
 QY 430 DLKESRPDSEGGKMTNPDR-----TTGEVK- YTHIAGDRDLKRYTVERPRTDTPDTFLK 481
 Db 411 ALSSV-----NKSTTVEQKPNERNNTANLQSMETN-----DTKNHTV-----EQTIYINP 456
 QY 482 IKVVEKGYREKGAAIEVSGLTE--TOLRAATOLAYFTDAAEL- DDKDLDKLYHGGD 537
 Db 457 LR-----SAKETVNUNLSGNGDEGSTIDSTIKVVKVGDMONLPPSNRVTYDSEED 510
 QY 538 MNDSTLAVAKILVEYAQDSNPPQLTDLDFIPNNKQYSLIGTQWHPEDLVIRMED- 595
 Db 511 VTND-----DQAQ-----LGNNNDVNINFGNIDSPY- IIVKSYKDPN 547
 QY 596 KKEVTPVTHNLTURKTVTGLAD----- 626
 Db 548 KDDYTTIQTQVTMOTNTINRYTGEERTASYDNTIAFSTSSQGQGDLPPKETVIGDVW 607
 QY 627 -----IELKNNKQBL-----SQTVKTDKUNLEFRDGKATINLKG--ESL 665
 Db 608 DVDKDGIQYNTDNEKPLSNAVLVITYPDGTSKSVRDRDEBGKQFQDG---LKNGLYKI 662
 QY 666 TQGSPGEGSYLVKET-----DSEGVYKVNSQEVANATV----- 700
 Db 663 TEE-TEPEGYTPTLKHSGTNPALDSEGSNSWVTINGQDDMTIDSGFYOPTPKYSLGNVYWW 721
 QY 701 -SKGIGTSDE-----TLAEN 715
 Db 722 TNKDGQGDEKGISGKVTLKD 746

RESULT 3
 US-10-617-320-3676
 Sequence 10, Application US/10617320
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Staam and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIA
 NUMBER OF SEQUENCES: 5206

Db 165 NG-----KIVNYYSDIDAHIAADANKNITKPVILPVGDIKKLEDTSIKYNG 212
 Qy 536 GDMNDSTLAVAKILVEYAQDSDNPOLTDIDFFTPNNKY---OSLIGHQ-HPELDVDI 590
 Db 213 GGTREVENGVN-----TQEVTPRMELNSTTIPENOFTTRIGYNLIG--WHHDKDLADT 264
 Qy 591 IRME-----DEKKEV-----PVTHNUTLKVUTGLADGRKDFHIEELKNN 632
 Db 265 GRVFTAGOSIGIDNNLDAINTLYAWQOPKEYTVGVSKVVGLEDKTDLFL-----N 318
 Qy 633 KOELLSQTWKTKDTNLEFFKGKATINLKGESESITLQGLIEGYSYLVKETDSEGKVKN 692
 Db 319 PSEFLQQ-----ENFPLDQGQ-TKEEK-----VPGTTSISIDECAYDEFKVSI 362
 Qy 693 QE-----VANATVSKTGTTS-----DETLAFENNEKEPVPTGVQDKI-----NG 731
 Db 363 TEKKLATGHDKTYDATGJQSLTVSGDVLIDSTN-----TRIKQKVRLQKVNVENDN 415
 Qy 732 YLA 734
 Db 416 FLA 418

RESULT 5
 PCR-US02/37235-44
 ; Sequence 44, Application PC/US0237235
 ; GENERAL INFORMATION:
 ; APPLICANT: Handfield, Martin
 ; APPLICANT: Hillman, Jeffrey
 ; APPLICANT: Proguiske Fox, Ann
 ; TITLE OF INVENTION: Identification of *Actinobacillus actinomycetemcomitans* Antigens
 ; TITLE OF INVENTION: In the Diagnosis, Treatment, and Monitoring of Periodontal Disease
 ; FILE REFERENCE: MBH01-662A
 ; CURRENT APPLICATION NUMBER: PCT/US02/37235
 ; NUMBER OF SEQ ID NOS: 234
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 44
 ; LENGTH: 1531
 ; TYPE: PRT
 ; ORGANISM: *Actinobacillus actinomycetemcomitans*
 PCT-US02-37235-44

Query Match 3.3%; Score 131.5; DB 1; Length 1531;
 Best Local Similarity 20.0%; Pred. No. 0.45; Mismatches 179; Conservative 120; Indels 275; Gaps 47;
 Qy 39 ALYTMVSGAKTVGVLVESTSPNAINPDS-----SEWRWYGYESYRGGHPYKQFRVAH 92
 Db 541 ANITATTNGSVDLG--NSTSTEGSHPSVNSSATVITYSGTGTKEGHSRVI--- 594
 Qy 93 DLRVNLEGSSRSYQYCFENKKAFLPLGSQDSVSKWYKHDGISTKFEDYAMSPLITGBLN 152
 Db 595 -----GSKGNERQIKW-AAGNVAANST-----DAVNGS-QLEAVASRY--EQG 634

Query Match 3.3%; Score 131; DB 1; Length 1456;
 Best Local Similarity 20.1%; Pred. No. 0.45; Mismatches 160; Conservative 126; Indels 248; Gaps 44;
 Matches 635 WQITSGVENGITGONGAASTATIKPSNOVQLLAGRNLAVERGKNTFTSTQENTFTNTT 694
 Qy 209 SNLVTSQSLIMQALKQ---LIDPLNLTAKMPQVDPDFQLSIFESEDKGKYN KGYQ 263
 Db 695 QDLTATGNTNVTKNEFSVQDNGTINMNRITITVAGTQDD-----DAVNFKQLK 742
 Qy 54 VESSTPN-----AINPDSSESYRWWGYESY--RGGHPYKQ---FVYADLNVNLE 99
 Db 466 VADSPLSRNNTLPALOSSN----VGSERHAPLEKDRPLVRESANFKVM-SLBRMD 519
 Qy 100 GSRSYQVY---CFNLKKAFPLGQSSSYKKWVKKHDLGIST-----FEDYAMS 143
 Db 520 EPAEQVNPQSOPENLRKFWDEANSNSKDNDKNITTSQKNSAPRNQKHEFSIKLS 579
 Qy 144 PRTGQ-ELNOKLRAVMNGHQ---INANGIMGLGE---PNARIA-TQEAWVYSSIN 195
 Db 580 GKNTHAEFLVLSPLRKVMAREMELNSKGILQVLPDETFPLSLR-----KYTYOLP 632
 Qy 356 IAEP-----TFKVEAGKVITI-----IDQKQIENPNKEVEPVSE 392
 Db 633 --GNESSESKENYEVN-----TEGIVTPVFEKEEDYSEOEIQUEST 671

PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: US09/598,042
 PRIOR FILING DATE: 2000-06-20
 PRIOR APPLICATION NUMBER: US09/620,312
 PRIOR FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: US09/553,450
 PRIOR FILING DATE: 2000-08-31
 PRIOR APPLICATION NUMBER: US09/662,191
 PRIOR FILING DATE: 2000-09-14
 PRIOR APPLICATION NUMBER: US09/693,036
 PRIOR FILING DATE: 2000-10-19
 PRIOR APPLICATION NUMBER: US09/727,344
 NUMBER OF SEQ ID NOS: 7143
 SOFTWARE: pt_FL_genes_b Versions 1.0
 SEQ ID NO: 2582
 LENGTH: 993
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-258-89A-2582

Query Match 3-28; Score 128; DB 6; Length 993;
 Best Local Similarity 20.1%; Pred. No. 0.43; Mismatches 145; Conservative 89; Mismatches 232; Indels 256; Gaps 35; Db 22 FKLFRLVKLLGGFDNIESGAVWKVY--QDYGIPVLSAAGYNYKCVKYY--LYGFE 75

Qy 85 YKOFYRAHDLR--VNLE-GSRSYQVQCFNLRKAFPL--GSDSSVWKWKKHDG1STKFE 138
 Db 139 DYAMSRPITGELNQKLRRAWVNGHQNANGIMEGLEPLNIRVOEAQWVYSDNAPIS 198
 Db 76 EYCRSPNT--EFQMLAPKEVKYNUCKOKECENYK-----IKVKEE----N 113
 Qy 199 PDE-SFRRESNLVYSTSQISLMRO-ALKQOLIDPNTAKMKPKQVDDFQLSIFESEDKG 255
 Db 114 ETEIQLIEKMEBERNIPPREERPLDIEERKENNIKPSLSK----- 153
 Qy 256 DKNYKGYQONLLSGLVPTKPPMPGDPMPNQPNQQTTSVLRKYAIGDYSKLEGATIQLT 315
 Db 154 -----KNNLES-----IPIHSDQEKEVENNIK-----P 175
 Qy 316 GDVNNSFQARVEFSSNDIGERIELSDGTYTTELNSPAGYSTAEPITFKVEAGKVYI 375
 Db 176 EDNEN-----LDDKDDTTRVD-----ESLNIVKEAEE----KA 206
 Qy 376 KOIENPNK-----ELVEPYSEAKDFEEFSVLTQNYAKFYAKNNG 419
 Db 207 KSGDNKEEDEDDEAEEEEEREEDEEDDNNEEPEECPYGMKQYRYGKGN- 265
 Qy 420 SSQVYVCFNADLKSPPDSEDGKTMTPDFTGEVKY-THIAGRDLRY-----TVKP 470
 Db 266 -QKMY-EASTK--DSDVEG-----GEVLYVHCGWNV-RYDENEKADKIVRP 308
 Qy 471 RDTDPDPELKHKKVTEGYERKGQIAEYSGLETQRLAATQALITYFTSAELDKKLK 530
 Db 309 ADKVNPK-IKRRKKINNLDKEKDKDKEKSP-KNCKLR-----RLSKPFPQ 352
 Qy 531 DYHGFDMNDSPLAVAKILVEQAQDSNPPQTLDFIPNNKQYOLIGTWHPELDKLK 590
 Db 353 -----TNPSPMVKLUDTDAKNSDTAHKSIET-----TSILINGQIQAASSED 397
 Qy 591 IRMEDKKEVIVPYTHNLTLRKTVTGLAGDRTKDFHFETELKNNKQELISQTVKTDKTNLREF 650
 Db 398 SEQEDERGAQDMNN-----GKEESKDH---LTNNRNDLISKEQNSSSLLE 443
 Qy 651 KDGKATNLKIGKESLTLQGLPEGYSILVKEKDSEGYKVQVNSOEVANATVS----- 701
 Db 444 NKVHADLWISKPVSKSPERLRKDIEVSEDTYEEDEVTKRKDVKDTDKSSKQIKR 503
 Qy 702 -----KLG-----ITSEDTLAFENN-----KEPVPTGQDKI 729
 Db 504 GKRRCYCNTECLKTGSPGKKEKAKKUKESLQMNENSSSSDEDEETKAKMPT--KY 560

RESULT 11
 US-10-408-765A-2576
 Sequence 2576 Application US/10408765A
 GENERAL INFORMATION:
 APPLICANT: Ghosh, Soumitra S.
 APPLICANT: Fahy, Eoin D.
 APPLICANT: Zhang, Bing
 APPLICANT: Gibson, Bradford W.
 APPLICANT: Taylor, Steven W.
 APPLICANT: Glenn, Gary M.
 APPLICANT: Warnock, Dale E.
 TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
 FILE REFERENCE: 660088 465
 CURRENT APPLICATION NUMBER: US/10/408,765A
 CURRENT FILING DATE: 2003-04-04
 NUMBER OF SEQ ID NOS: 3077
 SEQ ID NO: 2576
 LENGTH: 1090
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-408-765A-2576

Query Match 3-28; Score 128; DB 6; Length 1090;
 Best Local Similarity 18.3%; Pred. No. 0.49; Mismatches 153; Conservative 125; Mismatches 280; Indels 278; Gaps 42; Db 311 VYARVERRSVLLIEETIVN--NSNALESHEFYGAASESFQGIP-----I 356
 Qy 41 VTSMSVAKTIVGGLVVESTPNAINPDSSEYRKY---GYESYVRGHPYYQFRVADLRV 96
 Db 357 DISTRKKHOILF-KEENP-NNDITVLKGSTANFNKTPSVAPVNAKATISARFDPNKL 413
 Qy 152 NOKLRAWMYHNPQNANGIMEGLEPLNIRVQTOEAQWVYSDNAPISNPDSFKRSESNL 211
 Db 414 KTNLADAL--HSQS-----IIPPLEVNIPD-----DNLSETSKDTK-EANRASI 457
 Qy 212 VTSQSLSMRQALKOLIDPNTAKMKPKQVDDFQLSIFESEDKGDKYNNQYQNLSSGL- 270
 Db 458 IFTS---MNECTSTVDTVSTPSTSYVSQEDML--PGD--NYKSRGDFLNL 508
 Qy 271 -----VPTKRPPTGDPMPNQPNQQTTSVLRKYAIGDYSKLEGATIQLT--QLTGDNNSFQ 323
 Db 509 LLDLSNENPTEPG--LMRDNSFSESSI-----TRSEELERATEVGAINGGNYPEKQ 558
 Qy 324 ARVFSN---DIGERIELSDGTYTTELNSPAGYSTA---EPITFKVEAGKVY--- 371
 Db 559 VITQTNHSPYPLAWQVSPPIESTFSNNTPSDBSINFSPFSVNGNTPGNGETDEIVSKSQR 618
 Qy 372 -----IITDGKQ----- 377
 Db 619 AIEKAFSQIKESONSYVKIRKILANSQEDPATMEKLUSHETNTTVLIPAIKWPSSATKL 678
 Qy 378 --IENPNKEIVEPYSV-EAYNDFEE-----FSVLTQNYAKFYAKNNGSQVY 425
 Db 679 NLLNSNSDSDVDEEFHSEAGNSFSEPTSKLQDSDFVFKDTSFSKQAPPNLKGJSSVY 738
 Qy 426 CENADLUSPSPSDEG-----GKTMTP-----DFTTG-----EV 453
 Db 739 TSTLSEASRPNDQSSAFHIVSNTGRSSNTNTPARTLHGLQWRPTLPSDFTSMADPIYEL 798
 Qy 454 KYTHIAGRDLFK--YIVKPRD-----DPDFLKHKKVIEKGYR 491
 Db 799 TPVTPMQRDKTTRKDKDPSFLPCTTIPSQDVTLPITTSNSMASIFKENFK-HKDFI 856

Db 783 SPLQAKLAPVITGTNSKLEEGRFF---GKGIEQSHNTSADKRELLAPPVRD---ETP 834
 Qy 401 S-----VLTTONYAKFYAK-----NKQGSSQVWCNFADLKSPPD- 436
 Db 835 GNTALLKKAESGECOLSTONLQOMAAEDSHPLDPTSOLSRKGSE-----GDVASPPD 887
 Qy 437 -----SEDGKTMTP-----DFTT-----GEVKYHTAGRD 462
 Db 888 MLFPQDAHLVFOARVHPQSOTISETEKVLIPPRPLNDVSAQOKICGEWLSYFAGRE 947
 Qy 463 LFKYTKPRDTPDTLKKHKKVIEKGYREKGQAEVSGLUTETOLRATOLAIYFTDSA 522
 Db -----VPGEVNPE-FPEAVOPVC-----SPLNPPGVISPWATMDT 983
 Qy 523 ELDKDKLUKYHFGDMNDSTLAVAKLVEYAOQSNPQLTDFFIPNNNYQSLGT- 580
 Db 984 VPDR---KDFYSSNVYDPKTHEVGSYL---AQOMSPSDQ-----LSSFASTIVAQYG 1029
 Qy 581 QWHPEDLVDIIRMEDKKEVIVPVTNHLRKTVGLAGDRKDFP-HFETEIKN-NKQELL 637
 Db 1030 KGLPQEVEETVR---EDIWQPKSEFLEFASIGELEKTEFPEKSYEDPGNLVSKLI 1086
 Qy 638 SQTVKTDKTNLLEF---KOGKATNLKHGESELTLQGLPREGSYLVKE-TDSEGKVVKNSOE 694
 Db 1087 GSTEERRATSECHPEELKETVEKAAPLITESAFAFDAGFEKLKETIEAPPYQPOVSRE 1146
 Qy 695 VANATVSKTGITSDET 710
 Db 1147 ---ETHERESSESEQT 1159

RESULT 14
 US-09-200-650E-3
 Sequence 3, Application US/09200650E
 GENERAL INFORMATION:
 APPLICANT: Foster, Timothy J.
 APPLICANT: Hook, Magnus A.O.
 APPLICANT: Perkins, Samuel L.
 TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from *Staphylococcus aureus*
 FILE REFERENCE: P062830US2/RS
 CURRENT APPLICATION NUMBER: US/09/200, 650E
 CURRENT FILING DATE: 1998-11-25
 PRIOR APPLICATION NUMBER: 60/066, 815
 PRIOR APPLICATION NUMBER: 60/098, 427
 PRIOR FILING DATE: 1998-08-31
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 3
 LENGTH: 930
 TYPE: PRT
 ORGANISM: *Staphylococcus aureus*

US-09-200-650E-3

RESULT 15
 US-10-617-320-3251
 Sequence 3251, Application US/10617320
 GENERAL INFORMATION:
 APPLICANT: Lynn A. Douette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *STREPTOCOCCUS PNEUMONIAE* FOR DIAGNOSTICS
 NUMBER OF SEQUENCES: 5206
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 024354
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: <Unknown>
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: <Unknown>
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/617,320
 FILING DATE: 10-Jul-2003
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,433
 FILING DATE: 30-Jun-1998
 APPLICATION NUMBER: 60/085131
 FILING DATE: May 12, 1998
 APPLICATION NUMBER: 60/051553
 FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
 NAME: Arinella, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GRC-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3251:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1972 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 HYPOTHETICAL: YES

Db 226 YRIDSVSKEGDATTFKYGOYFRPGSVRLPSQNTQLYNAQGNIT--AKGIYDSTNTTY 282
 Qy 404 TTONYAKFY-----YAKKNKSS-QVVCNFADLKSPPDSD---GKIMTP 446
 Db 283 TETNIVQDQTNRGSEFOVAKRKRNMTDKYKMYTLDNTYSREIIVDYGNAQ 342
 Qy 447 DFTTGEVKYHTAGRDIFKTYVPRDT-DPDIFLKHKKVIEKGYREKGQAEYSSLT 505
 Db 343 LISSTNTINNEDLSRNMTPAVVNQPKNTYTKOFVTNL---TGYKFNPNAKFK--- 392
 Qy 506 QIRATOLAIYFTDSKLDKLUKQHFGDMNDSTLAVAKLVEYAOQSNPQLTD 565
 Db 393 -----IYEVTDQMF-----VDPWATMDT 404
 Qy 566 FFPNNNNYQSLIGTQWHPELDIIRMEDKKEVIVPVTNHLRKTVGLAGDRKDFH 625
 Db 405 STPDTSKLKD-----TOFDVYISNDK-----TATVULMKSGT----- 440
 Db 626 EELKNNKKOELLSO-----AVKTDKTNLEFKDGKATINLKHGESELTLQG 669
 Db 441 ---SSNKQYIQQAVPDNSSTDNGKIDYTDIDKTKYWSNSYSVN--GSSTANG 492
 Qy 670 LIEGYS---YAVKETDSEGYKVKNSCEVANVY---SKTGTSDELAENK 717
 Db 493 DOKYNLGDYWWBTDNKDG-KODANEKGKIGVYVILKDSNGKELDRTTDENGK 545

ORIGINAL SOURCE: ;
ORGANISM: Streptococcus pneumoniae
FEATURE: ;
NAME/KEY: misc-feature
LOCATION: (B) LOCATION 1..1972
SEQUENCE DESCRIPTION: SEQ ID NO: 3251:
ns-10-617-320-3251

Search completed: August 19, 2003, 15:29:15
Job time : 40 secs